

GenCore version 5.1.6  
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

run on: July 12, 2003, 20:35:11 ; Search time 1076 Seconds  
 (without alignments)  
 2434-250 Million cell updates/s

title:	US-09-910-757-1
perfect score:	90
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scoring table:	IDENTITY_NUC
	Gapop 10.0 , Gapext 1.0
searched:	2054640 seqs, 14551402878 residues
total number of hits satisfying chosen parameters:	
4109280	
minimum DB seq length:	0
maximum DB seq length:	2000000000
cost-processing: Minimum Match 0%	

## SUMMARIES

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	
		No.						
1	90	100.0	90	6	AR176162	Sequence	AR176162 Sequence	
2	90	100.0	256	9	HDMPPRAPP		M35675 Human amylo	
3	90	100.0	1154	9	HUMAMPTP01		M31862 Human amylo	
4	90	100.0	1286	9	HUMAPPB01		M24546 Human beta-	
5	90	100.0	1319	9	BC004369		BC004369 Homo sapi	
6	90	100.0	3353	6	A02759		I36121 H. sapiens m	
7	90	100.0	3353	6	I36121	Sequence 1	I36121 Sequence 1	
8	90	100.0	3353	6	I66657	Sequence 12	I66657 Sequence 12	
9	90	100.0	3354	6	AX026822	Sequence	AX026822 Sequence	
10	90	100.0	3354	9	HSAFPAP4		Y00264 Human mRNA	
11	90	100.0	8591	6	I58322	Sequence	I58322 Sequence	
12	90	100.0	8591	6	I58323	Sequence	I58323 Sequence	
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14	90	100.0	8591	6	I60509	Sequence 8	I60509 Sequence 8	
15	90	100.0	8591	6	I77052	Sequence 6	I77052 Sequence 6	
16	90	100.0	8591	6	I77053	Sequence 8	I77053 Sequence 8	
17	90	100.0	8591	6	I87173	Sequence 6	I87173 Sequence 6	
18	90	100.0	8591	6	I87174	Sequence 8	I87174 Sequence 8	
19	90	100.0	83661	9	AP001439		AP001439 Homo sapi	
c	c	20	90	100.0	100000	9	AP000143	AP000143 Homo sapi
c	c	21	90	100.0	120634	9	AP001594	AP001594 Homo sapi
c	c	22	90	100.0	121597	9	AP000090	AP000090 Homo sapi
c	c	23	90	100.0	123631	9	HS22FB01	AL109967 Homo sapi
c	c	24	90	100.0	301692	9	D87675	D87675 Homo sapien
c	c	25	90	100.0	340000	9	AP001695	AP001695 Homo sapi
c	c	26	88.4	98.2	3148	6	I36122	I36122 Sequence
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c	c	28	88.4	98.2	3520	6	AR072114	AR072114 Sequence
c	c	29	78.2	86.9	3098	9	MACABPKP1B	M58727 M. fascicula
c	c	30	78.2	86.9	6074	9	AF067971	AF067971 Macaca mu
c	c	31	66	73.3	1286	6	AX347152	AX347152 Sequence
c	c	32	58	64.4	2340	9	S81024	S81024 beta- PP751
c	c	33	51.8	57.6	1286	6	AX347153	AX347153 Sequence
c	c	34	50	55.6	3804	6	AR068368	AR068368 Sequence
c	c	35	50	55.6	3804	9	HSPADP	X12751 Human prmt
c	c	36	49.8	55.3	3111	10	CSAMYLOID	X97631 Cavia sp. m
c	c	37	46.6	51.8	1361	10	MUSALABA	D10603 Mus musculu
c	c	38	45	50.0	2360	6	E02400	E02400 DNA encodin
c	c	39	42.2	46.9	2520	10	MGSABPPA	M18373 Mouse amylo
c	c	40	42.2	46.9	2520	10	MDP84012	M84012 Mus musculu
c	c	41	38.4	42.7	105620	2	AC127760	AC127760 Rattus no
c	c	42	37	41.1	1556	6	AX205669	AX205669 Sequence
c	c	43	37	41.1	499	10	RATAPPG	L11926 Rat amyloid
c	c	44	37	41.1	157649	2	AC094616	AC094616 Rattus no
c	c	45	37	41.1	180010	2	AC120935	AC120935 Rattus no

ALIGNMENTS

RESULT 1  
 AR176162  
 LOCUS DEFINITION  
 ACCESSION NUMBER  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCES  
 AUTHOR

29:  
 em\_v1: \*  
 30: em\_htg\_hum: \*  
 31: em\_htg\_inv: \*  
 32: em\_htg\_other: \*  
 33: em\_htg\_mus: \*  
 34: em\_htg\_pln: \*  
 35: em\_htg\_rod: \*  
 36: em\_htg\_ram: \*  
 37: em\_htg\_vrt: \*  
 38: em\_sy: \*  
 39: em\_htgo\_hum: \*  
 40: em\_htgo\_mus: \*

Pred. No. is the number of results predicted by chance to have

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source	1..90 /organism="unknown"
BASE COUNT	14 a 30 c 40 g 6 t
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Qy	1 GGGAGACGGGGGGCGCTGGGGCGAGGACAAAGGACGGGGATCCCACTCGGACA 60 
Db	1 GGGAGACGGGGCGGTGGGGCGAGGACAAAGGACGGGGATCCCACTCGGACA 60 
Qy	61 GCAAGCAGACTCGTGCCTGCCAGGGTCG 90 
Db	61 GCAAGCAGACTCGTGCCTGCCAGGGTCG 90 
RESULT 2	
HUMPRAPP	HUMPRAPP 256 bp mRNA linear PRI 08-JAN-1995
LOCUS	Human amyloid beta precursor protein (ABPP) mRNA, 5' end.
DEFINITION	
ACCESSION	M35675
VERSION	M35675.1 GI:190306
KEYWORDS	amyloid beta.
ORGANISM	Homo sapiens
DEFINITION	Human fetal muscle, cDNA to mRNA, clone lambda-HAP2.
ACCESSION	M35675.1 GI:190306
VERSION	1 (bases 1 to 256)
KEYWORDS	Human; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	Mita,S., Sadlock,J., Herbert,J. and Schon,E.A.
AUTHORS	
TITLE	A cDNA specifying the human amyloid beta precursor protein (ABPP) encodes a 95-kDa polypeptide Nucleic Acids Res. 16 (19), 9351 (1988)
JOURNAL	
MEDLINE	89016647
PUBMED	2191912*
FEATURES	
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gene	1..256 /gene="APP"
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Qy	1 GGGAGACGGGGGGCGCTGGGGCGAGGACAAAGGACGGGGATCCCACTCGGACA 60 
Db	135 GGGAGACGGGGGGCGCTGGGGCGAGGACAAAGGACGGGGATCCCACTCGGACA 194 
Qy	61 GGGAGACGGGGGGCGCTGGGGCGAGGAC 90 
Db	195 GGGAGACGGGGGGCGCTGGGGCGAGGAC 224 
RESULT 3	
HUMAPPB01	HUMAPPB01 1286 bp DNA linear PRR 31-OCT-1994
LOCUS	Human beta-amyloid protein (beta-APP) gene, exon 1.
DEFINITION	
ACCESSION	M24546.1 GI:341201
VERSION	1 of 2
SEGMENT	
SOURCE	Homo sapiens (tissue library: of Young) DNA.
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1286)
AUTHORS	La Fauci,G., Lahiri,D.K., Salton,S.R. and Robakis,N.K.
TITLE	Characterization of the 5'-end region and the first two exons of

the beta protein precursor gene	
JOURNAL	Biochem. Biophys. Res. Commun.
MEDLINE	159 (1), 297-304 (1989)
PubMed	89165870
PubmedID	2538123
FEATURES	Location/Qualifiers
Source	<p>1. .1286 /organism="Homo sapiens"            /db_xref="taxon:9606"            /map="21q21.2"            /tissue_idb="of young"</p> <p>protein_bind /bound_moiety="SP1"            repeat_unit 177. .186 /rpt_type=direct            repeat_unit 177. .186 /rpt_type=direct            TATA_Signal 102. .206            repeat_unit 212. .221            repeat_unit 212. .221 /rpt_type=direct            repeat_unit 523. .531 /rpt_type=direct            misc_feature 523. .531 /rpt_type=direct            repeat_unit 547. .553 /bound_moiety="AP1"            misc_feature 580. .593 /note="heat shock element"            repeat_unit 638. .646 /rpt_type=direct            repeat_unit 638. .646 /rpt_type=direct            GC_signal 710. .715            GC_signal 737. .742            GC_signal 752. .757            GC_signal 759. .764            exon 768. .1103 /gene="APP"            /note="minor transcription start site; G00-119-692            /number_1</p> <p>GC_signal 787. .792 /gene="APP"            exon 833. .1103 /gene="APP"            /note="minor transcription start site; G00-119-692            /number_1</p> <p>protein_bind 855. .861 /bound_moiety="AP1"            stem_loop 873. .897 /gene="APP"            /note="sequence capable of forming a hairpin-like            structure"            exon 895. .1103 /gene="APP"            /note="minor transcription start site; G00-119-692            /number_1</p> <p>exon 899. .1103 /gene="APP"            /note="major transcription start site; G00-119-692            /number_1</p> <p>exon 907. .1103 /gene="APP"            /note="minor transcription start site; G00-119-692            /number_1</p> <p>exon 917. .1103 /gene="APP"            /note="minor transcription start site; G00-119-692            /number_1</p> <p>repeat_unit 934. .1103 /gene="APP"            /note="minor transcription start site; G00-119-692            /number_1</p> <p>repeat_unit 951. .959 /gene="APP"</p>

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Qy 1 GGGAGACGGCGGGTGGCGGGCAGGACAAAGGACGGGGATCCACTCGCAC 60
Db 955 GGGAGACGGCGGGTGGCGGGCAGGACAAAGGACGGGGATCCACTCGCAC 101
Qy 61 GCAGGCCACTCGGTGCCGGCAGGGTCG 90
Db 1015 GCAGGCCACTCGGTGCCGGCAGGGTCG 1044

RESULT 5
BC004369 LOCUS BC004369 1319 bp mRNA linear PRI 12-JUL-200
DEFINITION Homo sapiens, Similar to amyloid beta (A4) precursor protein
(prototype nevin-II, Alzheimer disease), clone MGC:10403
IMAGE:3619593, mRNA, complete cds.
ACCESSION BC004369
VERSION BC004369.1 GI:13325111
KEYWORDS MGC.
ORGANISM Homo sapiens.
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE Strausberg,R.
AUTHORS Submitted (12-MAR-2001). National Institutes of Health, Mammalian
TITLE Direct Submission
JOURNAL Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgaps-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bogsc.bc.ca
Steven Jones, Jennifer Asano, Ian Boddet, Yaron Butterfield,
Susanna Chan, Reedman Chan, Chris Fiehl, Erin Garland, Ron Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Loraine Spence, Jeff Scott,
Michael Thorne, Miranda Tsai, Natasha van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LILNL at: http://image.llnl.gov
Series: IRAL Plate:13 Row: j Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4502166.
Location/Qualifiers
FEATURES Source
1. .1319
Organism="Homo sapiens"
db_xref="taxon:9604"
clone="MGC_10403"
IMAGE:3619593

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 QY 1 GGGAGACGGCGGCCGTTGGCCGGCGAGCAAGAGCAGCGGCCACTCGCACA 60  
 Db 35 GGGAGACGGCGGCCGTTGGCCGGCGAGCAAGAGCAGCGGCCACTCGCACA 94

QY 61 GCAGCGCACTCGGTGCCCGCGCAGGGTCG 90  
 Db 95 GCAGCGCACTCGGTGCCCGCGCAGGGTCG 124

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RESULT 6  
 A02759 LOCUS A02759 H.sapiens mRNA for amyloid plaque core protein.  
 DEFINITION H.sapiens mRNA for amyloid plaque core protein.  
 ACCESSION A02759  
 VERSION A02759..1 GI:345130  
 KEYWORDS SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrate; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.  
 REFERENCE Mueller-Hill, B.; Kang, J.; Lemaire, H.G., and Unterbeck, A.  
 AUTHORS  
 TITLE Precursor Protein of APP polypeptide, DNA coding therefor and  
 diagnostic use of the DNA and protein  
 Patent: EP 0276723-A 1 03-AUG-1988;  
 BAYER AG  
 FEATURES Location/Qualifiers  
 source 1..3353  
 /organism="Homo sapiens"  
 /db\_xref="Taxon:9606"  
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 /db\_xref="GI:345131."  
 /db\_xref="SWISS-PROT:IP05067"  
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 BASE COUNT 922 a 745 c 867 g 819 t

ORIGIN

RESULT 7  
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 ACCESSION I36121  
 VERSION I36121..1 GI:2087345  
 KEYWORDS SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 3353)  
 AUTHORS Wadsworth, S., Snyder, B., Reddy, V.B. and Wei, C.  
 TITLE cDNA-geneomic DNA hybrid sequence encoding AP770 containing a genomic DNA insert of the K1 and OX-2 regions  
 Patent: US 5604131-A 1 18 FEB 1997;  
 JOURNAL FEATURES Location/Qualifiers  
 SOURCE 1..3353  
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 BASE COUNT 922 a 745 c 867 g 819 t

ORIGIN

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 Db 55 GGAGACGGCGGCCGTTGGCCGGAGAGCAGAAAGCAGCGGCCACTCGCACA 114

QY 61 GCAGCGCACTCGGTGCCCGCGCAGGGTCG 90  
 Db 115 GCAGCGCACTCGGTGCCCGCGCAGGGTCG 144

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RESULT 8  
 I66657 LOCUS I66657  
 DEFINITION Sequence 12 from patent US 5670634.  
 ACCESSION I66657  
 VERSION I66657..1 GI:2724635  
 KEYWORDS SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 3353)  
 AUTHORS Marotta, C.A., Majocha, R.E. and Agrawal, S.  
 TITLE Reversal of .beta.-amyloid peptide induced morphological changes in neuronal cells by antisense oligonucleotides  
 Patent: US 5670634-A 12 23-SEP-1997;  
 JOURNAL FEATURES Location/Qualifiers  
 SOURCE 1..3353  
 /organism="unknown"  
 BASE COUNT 922 a 745 c 867 g 819 t

ORIGIN





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Search completed: July 12, 2003, 21:33:47  
Job time : 1080 secs